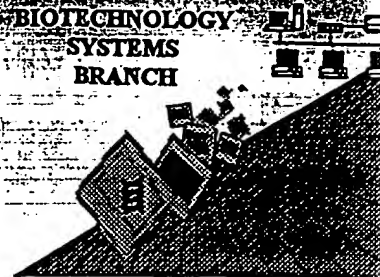# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/150 947 A_

Art Unit / Team No. : _1645_

Date Processed by STIC: _6 - 8 - 00_

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/150,947A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid
Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
(NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
(NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" _
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1645

RAW SEQUENCE LISTING   DATE: 06/08/2000
PATENT APPLICATION: US/09/150,947A   TIME: 08:04:01

Input Set : A:\A31967-PCT-USA seq list.txt
Output Set: N:\CRF3\06082000\I150947A.raw

```
 4 <110> APPLICANT: Raymond Kaempfer
 5       Gala Arad
 7 <120> TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
 8       ANTAGONISTS AND VACCINES
11 <130> FILE REFERENCE: A31967-PCT-USA-A
13 <140> CURRENT APPLICATION NUMBER: 09/150,947A
14 <141> CURRENT FILING DATE: 1998-09-10
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 26
22 <212> TYPE: PRT
23 <213> ORGANISM: Staphylococcal aureus
25 <400> SEQUENCE: 1
26  Ser Glu Gln Glu Asn Cys Glu Leu Ile Ser Thr Ile Asn Gly Thr Asn
27  1               5                  10                  15
28  Lys Lys Lys Val Thr Ala Gln Glu Leu Asp
29            20                  25
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 12
33 <212> TYPE: PRT
34 <213> ORGANISM: Staphylococcal aureus
36 <400> SEQUENCE: 2
37  Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
38  1               5                  10
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 10
42 <212> TYPE: PRT
43 <213> ORGANISM: Staphylococcal aureus
45 <220> FEATURE:
46 <221> NAME/KEY: VARIANT
47 <222> LOCATION: (0)...(0)
49 <400> SEQUENCE: 3
50  Lys Lys Lys Val Thr Ala Gln Glu Leu Asp
51  1               5                  10
53 <210> SEQ ID NO: 4
54 <211> LENGTH: 10
55 <212> TYPE: PRT
56 <213> ORGANISM: Staphylococcal aureus
58 <400> SEQUENCE: 4
59  Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
60  1               5                  10
62 <210> SEQ ID NO: 5
63 <211> LENGTH: 13
64 <212> TYPE: PRT
65 <213> ORGANISM: Staphylococcal aureus
67 <220> FEATURE:
```

```
           RAW SEQUENCE LISTING              DATE: 06/08/2000
           PATENT APPLICATION:  US/09/150,947A      TIME: 08:04:01

              Input Set : A:\A31967-PCT-USA seq list.txt
              Output Set: N:\CRF3\06082000\I150947A.raw

     68 <223> OTHER INFORMATION: n-lauryl cysteine residue
     70 <400> SEQUENCE: 5
     71   Xaa Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp
     72   1               5                   10
     74 <210> SEQ ID NO: 6
     75 <211> LENGTH: 13
     76 <212> TYPE: PRT
     77 <213> ORGANISM: Staphylococcal aureus
     79 <220> FEATURE:
     80 <223> OTHER INFORMATION: n-lauryl cysteine
     82 <400> SEQUENCE: 6
     83   Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
     84   1               5                   10
     86 <210> SEQ ID NO: 7
     87 <211> LENGTH: 16
     88 <212> TYPE: PRT
     89 <213> ORGANISM: Staphylococcal aureus
     91 <400> SEQUENCE: 7
     92   Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys
     93   1               5                   10                  15
     95 <210> SEQ ID NO: 8
     96 <211> LENGTH: 35
     97 <212> TYPE: PRT
     98 <213> ORGANISM: Staphylococcal aureus
    100 <400> SEQUENCE: 8
    101   Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys
    102   1               5                   10                  15
    103   Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys Lys Ala Thr Val
    104               20                  25                  30
    105   Glu Leu Asp
    106               35
    108 <210> SEQ ID NO: 9
    109 <211> LENGTH: 14
    110 <212> TYPE: PRT
    111 <213> ORGANISM: Staphylococcal aureus
    113 <220> FEATURE:
    114 <221> NAME/KEY: DISULFID
    115 <222> LOCATION: (1)...(1)
    117 <221> NAME/KEY: DISULFID
    118 <222> LOCATION: (14)...(14)
    120 <221> NAME/KEY: DISULFID
    121 <222> LOCATION: (14)...(14)
    123 <400> SEQUENCE: 9
    124   Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa
    125   1               5                   10
    127 <210> SEQ ID NO: 10
    128 <211> LENGTH: 14
    129 <212> TYPE: PRT
    130 <213> ORGANISM: Staphylococcal aureus
```

[handwritten annotations:] No <222>: Numerical Location of Xaa's within Sequence. See Error Summary Sheet, #10

delete "c"

These describe bonds, but no explanation of what Xaa's represent. Xaa can only represent a single amino acid, nothing else. duplicated—see above

```
132 <220> FEATURE:
133 <223> OTHER INFORMATION: D-alanine residue
135 <223> OTHER INFORMATION: D-alanine residue
137 <400> SEQUENCE: 10
138 Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa
139 1               5                   10
141 <210> SEQ ID NO: 11
142 <211> LENGTH: 14
143 <212> TYPE: PRT
144 <213> ORGANISM: Staphylococcal aureus
146 <220> FEATURE:
147 <223> OTHER INFORMATION: N-acetyl group
149 <223> OTHER INFORMATION: D-alanine residue
151 <400> SEQUENCE: 11
152 Xaa Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Xaa
153 1               5                   10
155 <210> SEQ ID NO: 12
156 <211> LENGTH: 239
157 <212> TYPE: PRT
158 <213> ORGANISM: Staphylococcal aureus
160 <400> SEQUENCE: 12
161 Glu Ser Gln Pro Asp Pro Lys Pro Asp Glu Leu His Lys Ser Ser Lys
162 1               5                   10                  15
163 Phe Thr Gly Leu Met Glu Asn Met Lys Val Leu Tyr Asp Asp Asn His
164             20                  25                  30
165 Val Ser Ala Ile Asn Val Lys Ser Ile Asp Gln Phe Leu Tyr Phe Asp
166             35                  40                  45
167 Leu Ile Tyr Ser Ile Lys Asp Thr Lys Leu Gly Asn Tyr Asp Asn Val
168         50                  55                  60
169 Arg Val Glu Phe Lys Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys
170 65                  70                  75                  80
171 Tyr Val Asp Val Phe Gly Ala Asn Tyr Tyr Tyr Gln Cys Tyr Phe Ser
172             85                  90                  95
173 Lys Lys Thr Asn Asp Ile Asn Ser His Glu Thr Asp Lys Arg Lys Thr
174             100                 105                 110
175 Cys Met Tyr Gly Gly Val Thr Glu His Asn Gly Asn Gln Leu Asp Lys
176         115                 120                 125
177 Tyr Arg Ser Ile Thr Val Arg Val Phe Glu Asp Gly Lys Asn Leu Leu
178     130                 135                 140
179 Ser Phe Asp Val Gln Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu
180 145                 150                 155                 160
181 Asp Tyr Leu Thr Arg His Tyr Leu Val Lys Asn Lys Lys Leu Tyr Glu
182             165                 170                 175
183 Phe Asn Asn Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Asn
184         180                 185                 190
185 Glu Asn Ser Phe Trp Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe
186         195                 200                 205
187 Asp Gln Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn Lys Met Val Asp
188     210                 215                 220
```

Error: #10

Xaa can only represent a single amino acid, Error #10 nothing else.

RAW SEQUENCE LISTING   DATE: 06/08/2000
PATENT APPLICATION: US/09/150,947A   TIME: 08:04:01

Input Set : A:\A31967-PCT-USA seq list.txt
Output Set: N:\CRF3\06082000\I150947A.raw

```
189  Ser Lys Asp Val Lys Ile Glu Val Tyr Leu Thr Thr Lys Lys Lys
190  225             230             235
```

VERIFICATION SUMMARY   DATE: 06/08/2000
PATENT APPLICATION: US/09/150,947A TIME: 08:04:02

Input Set : A:\A31967-PCT-USA seq list.txt
Output Set: N:\CRF3\06082000\I150947A.raw

```
L:71  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:71  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:71  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:83  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:83  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:83  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:124 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:124 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:138 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:138 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:138 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:152 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:152 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:152 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
```